	Figure 1:	
_	PREF-1 SCS0009	MIATGALLRVLLLLLAFGHSTYGAECDPPCDPQYGFCEADNVCRCHVGWEGPLCDKC MPSGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC * * * * * * * * * * * * * * * * * * *
5	PREF-1 SCS0009	VTAPGCVNGVCKEPWQCICKDGWDGKFCEIDVRACTSTPCANNGTCVDLEKGQYECSCTP VRMPGCQHGTCHQPWQCICHSGWAGKFCDK
10		Additional exon coding for 30 aa is inserted in SECP59 (INCYTE WO0226982) HKAAV61 (HGS WO0134768) PRO40 (GENENTECH WO0224888) PREF-1 (HYSEQ WO0157233 LP230S (LILLY WO0248361) AAG67516 (SKB WO0166690 35.31 (BIODOOR WO0226809)
15	PREF-1 SCS0009	GFSGKDCQHKAGPCV INGSPCQHGGACVDDEGQASHASCLCPPGFSGNFCEIVAATNSCT GFHGRDCERKAGPCEQAGSPCRNGGQCQDDQGFALNFTCRCLVGFVGARCEVNVDDCL ** * * * * * * * * * * * * * * * * * *
20	PREF-1 SCS0009	PNPCENDGVCTDIGGDFRCRCPAGFVDKTCSRPVSNCAS GPCQNGGTCLQHTQVSFECLC MRPCANGATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHD -FDCLC ** * * * * * * * * * * * * * * * * *
25		1 Met in NOV8 EN WOO255704)
30	PREF-1 SCS0009	KPPFMGPTCAKKRGAS -PVQVTHLPSGYGLTYRLTPGVHELPVQQPEQHILKVSMKELN PSGYGGKTCELVLPVPDPPTTVDTPLGP -TSAVVVPATGPAPHSAG -AGLLRISVKEVVR . * * * * * * * * * * * * * * * * * * *
35	PREF-1 SCS0009	KSTPLLTEGQAICFTILGVLTSLVVLGTVAIVFLNKCETWV SNLRYNHTFRKKKNLLLQY RQEAGLGEPSLVALVVFGALTAALVLATVLLTLRAWRRGVCPPGPCCYPAPHYAPA . * * * ** ** ** *
33	PREF-1 SCS0009	NSGEELAVNIIFPEKIDMTTFNKEAGDEEI - CQDQECQVSMLPAGLPL PRDLPPEPGKTTAL .* * * *
40		

- 2/36 -

Figure 2:

Clustal W alignment of predicted amino acid sequences of SCS0009 prediction and splice variants SV3, SV4 and SV5.

5 CLUSTAL W (1.83) multiple sequence alignment

10	SV4 SV5 SV3 SCS0009	MP SGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC MPSGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC MPSGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC MPSGCRCLHLVCLLCILGAPGQPVRAD DCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC ***********************************
15	SV4 SV5 SV3 SCS0009	VRMPGCQHGTCHQPWQCICHSGWAGKFCDKDEHICTTQSPCQNGGQCMYDGGGEYHCVCL VRMPGCQHGTCHQPWQCICHSGWAGKFCDKDEHICTTQSPCQNGGQCMYDG GGEYHCVCL VRMPGCQHGTCHQPWQCICHSGWADEHICTTQSPCQNGGQCMYDGGGEYHCVCL VRMPGCQHGTCHQPWQCICHSGWAGKFCDK
20	SV4 SV5 SV3 SCS0009	PGFHGRDCERKAGP
25	SV4 SV5 SV3 SCS0009	RPCANGATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPS RPCANGATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPS RPCANGATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARC RDRVHDFDCLCPS
30	SV4 SV5 SV3 SCS0009	GYGGKTCELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEA GYGGKTCELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEA GYGGKTCELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEA

35

Figure 3:

Clustal W alignment of precited amino acid sequences of SCS0009 with SV1 and SV2

5	scs0009	MPSGCRCLHLVCLLCILGAPG QPVRA
	SV1-ORF	
	SV2-ORF	
10	scs0009	DDCSSHCDLAHGCCAPDGSC RCDPGWEGLHCERCVRMPGCQHGTCHQPWQCICHSGWAGK
	SV1-ORF	MPGCQHGTCHQPWQCICHSGWAGK
	SV2-ORF	MPGCQHGTCHQPWQCICHSGWA ***********************************
15		CHUCO DORDAYA C DOROAC C DOBNICO
	SCS0009	FCD K GFHGRDCERKAG PCEQAGSPCRNGG
	SV1-ORF	FCDKDEHICTTQSPCQNGGQCMYDGGGEYHCVCLPGFHGRDCERKAGPCEQAGSPCRNGG
	SV2-ORF	DEHICTTOSPCONGGOCMYDGGGEYHCVCLPGFHGRDCERKAGPCEQAGSPCRNGG
20		
	scs0009	QCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANGATCLDGINRFSCLCPEGFAG
	SV1-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANGATCLDGINRFSCLCPEGFAG
	SV2-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANGATCLDGINRFSCLCPEGFAG
25		*************
	scs0009	RFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKTCELVLPVPDPPTTVDTPLGP
	SV1-ORF	RFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKTCELVLPVPDPPTTVDTPLGP
	SV2-ORF	RFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKTCE LVLPVPDPPTTVDTPLGP
30		**************
	scs0009	TSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEAGLGEPSLVALVVFGALTAALVLATVL
	SV1-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEAGLGEPSLVALVVFGALTAALVLATVL
	SV2-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEAGLGEPSLVALVVFGALTAALVLATVL
35		*****
	scs0009	LTLRAWRRGVCPPGPCCYPAPHYAPACQDQECQVSMLPAGLPLPRDLPPEPGKTTAL .
	SV1-ORF	I.TLRAWRRGVCPPGP CCYPAPHYAPACQDQECQVSMLPAGLPLPRDLPPEPGKTTAL .
	SV2-ORF	LTLRAWRRGVCPPGPCCYPAPHYAPACQDQECQVSMLPAGLPLPRDLPPEPGKTTAL .
40		**************

XY = exon boundaries.

45 In the translation, the SV1 and SV2 se quences are shown representing the longest ORF available.

The predicted signal peptide of SCS0009 is shown highlighted in $\,$ yellow. The SV1 and SV2 longest ORFs do not contain predicted signal peptides.

50

- 4/36 -

Figure 4:

Nucleotide sequence of SCS0009 prediction with translation

5	1 61 121	AGACGGCAAC GTGGACAGGA AGAAGCGGAG GGCGAGGAGG AGCAGAGGAG CACACAGATG AAGCAGGTGT CCACGCGTCC GGCCGTCCAT CCGTCCGTCC CTCCTGGGGC CGGCGCTGAC CATGCCCAGC GGCTGCCGT GCCTGCATCT CGTGTGCCTG TTGTGCATTC TGGGGGCTCC
		MPSGCRCLHLVCL LCI LGA
10	181	CGGTCAGCCT GTCCGAGCCG ATGACTGCAG CTCCCACTGT GACCTGGCCC ACGGCTGCTG P G Q P V R A D D C S S H C D L A H G C
1.5	241	TGCACCTGAC GGCTCCTGCA GGTGTGACCC GGGCTGGGAG GGG CTGCACT GTGAGCGCTG C A P D G S C R C D P G W E G L H C E R
15	301	TGTGAGGATG CCTGGCTGCC AGCACGGTAC CTGCCACCAG CCATGGCAGT GCATCTGCCAC V R M P G C Q H G T C H Q P W Q C I C
20	361	CAGTGGCTGG GC AGGCAAGT TCTGTGACAA AGGCTTCCAT GGGCGTGACT GCGAGCGCAA H S G W A G K F C D K G F H G R D C E R
	421	GGCTGGACCC TGTGAACAGG CAGGCTCCCC ATGCCGCAAT GGCGGGCAGT GCCAGGACGA K A G P C E Q A G S P C R N G G Q C Q D
25	481	CCAGGGCTTT GCTCTCAACT TCACGTGCCG CTGCTTGGTG GGCTTTGTGG GTGCCCGCTG D Q G F A L N F T C R C L V G F V G A R
20	541	TGAGGTAAAT GTGGATGACT GCCTGATGCG GCCTTGTGCT AACGGTGCCA CCTGCCTTGAC E V N V D D C L M R P C A N G A T C L
30	601	CGGCATAAAC CGCTTCTCCT GCCTCTGTCC TGAGGGCTTT GCTGGACGCT TCTGCACCAT D G I N R F S C L C P E G F A G R F C T
35	661	CAACCTGGAT GACTGTGCCA GCCGCCCATG CCAGAGAGGG GCCCGCTGTC G GGACCGTGT I N L D D C A S R P C Q R G A R C R D R
	721	CCACGACTTC GACTGCCTCT GCCCCAGTGG CTATGGTGGC AAGACCTGTG AGCTTGTCTT V H D F D C L C P S G Y G G K T C E L V
40	781	ACCTGTCCCA GACCCCCCAA CCACAGTGGA CACCCCTCTA GGGCCCACCT CAGCTGTAGT L P V P D P P T T V D T P L G P T S A V
45	841	GGTACCTGCC ACGGGGCCAG CCCCCACAG CGCAGGGGCT GGTCTGCTGC GGATCTCAGT V V P A T G P A P H S A G A G L L R I S
43	901	GAAGGAGGTG GTGCGGAGGC AAGAGGCTGG GCTAGGTGAG CCTAGCTTGG TGGCCCTGGT V K E V V R R Q E A G L G E P S L V A L
50	961	GGTGTTTGGG GCCCTCACTG CTGCCCTGGT TCTGGCTACT GTGTTGCTGA CCCTGAGGGC V V F G A L T A A L V L A T V L L T L R
	1021	CTGGCGCCGG GGTGTCTGCC CCCCTGGACC CTGTTGCTAC CCTGCCCCAC ACTATGCTCC A W R R G V C P P G P C C Y P A P H Y A
55	1081	AGCGTGCCAG GACCAGGAGT GTCAGGTTAG CATGCTGCCA GCAGGGCTCC CCCTGCCACG PACQDQECQVSMLPAGLPLP
60	1141	TGACTTGCCC CCTGAGCCTG GAAAGACCAC AGCACTGTGA TGGAGGTGGG GGCTTTCTGG

- 5/36 -

5	1261 1321 1381 1441 1501 1561	CTTGGGTACA ACAGAATGTA CCAGAAAAAC GGAAGCCTCA TTTCCCTTCT AGCACCTCTG	CACACAGAGG AGATGGAATT CCACCTGGCG GGATGC TGCC GGGGAAGTGT TATAGGCCCG	AGACCTCAGC TTATCAAATA TTCCAGATGC CACCAAGGAG GGAGAGGTAG GCCTGGATCA	CTCACACCAG AAACTATGAA AAGAGGGCCA TGATTTCCAA AGCCCCAGAG GAGAGAGGGG	AAATATTATT AATGCAAGTG GAGCAGAGGC AGAGTAATCC GAGAATGTAA AGAACTCTGC	GGCTCCTATG CTGGTTCTGG AGGGTGCCCT ACAAGCAGCC
	1621	ATTGGGCTCA	GGGACCTCCG	AGTGAGGCAG	GGACTCCCTG	CTG	

- 6/36 -

Figure 5:

Nucleotide sequence with translation of cDNA insert in image clone 5478078 (SCS0009 -SV3)

5	1	ATGCCCAGCG GCTGCCGCTG CCTGCATCTC GTGTGCCTGT TGTGCATTCT GGGGGCTCCC
	•	M P S G C R C L H L V C L L C I L G A P
10	61	GGTCAGCCTG TCCGAGCCGA TGACTGCAGC TCCCACTGTG ACCTGGCCCA CGGCTGCTGT G Q P V R A D D C S S H C D L A H G C C
	121	GCACCTGACG GCTCCTGCAG GTGTGACCCG GGCTGGGAGG GGCTGCACTG TGAGCGCTGT A P D G S C R C D P G W E G L H C E R C
15	181	GTGAGGATGC CTGGCTGCCA GCACGGTACC TGCCACCAGC CATGGCAGTG CATCTGCCAC V R M P G C Q H G T C H Q P W Q C I C H
20	241	AGTGGCTGGG CAGATGAACA TATCTGTACC ACGCAGTCCC CCTGCCAGAA TGGAGGCCAG S G W A D E H I C T T Q S P C Q N G G Q
20	301	TGCATGTATG ACGGGGGCGG TGAGTACCAT TGTGTGTGCT TACCAGGCTT CCATGGGCGT C M Y D G G E Y H C V C L P G F H G R
25	361	GACTGCGAGC GCAAGGCTGG ACCCTGTGAA CAGGCAGGCT CCCCATGCCG CAATGGCGGG D C E R K A G P C E Q A G S P C R N G G
	421	CAGTGCCAGG ACGACCAGGG CTTTGCTCTC AACTTCACGT GCCGCTGCTT GGTGGGCTTT Q C Q D D Q G F A L N F T C R C L V G F
30	481	GTGGGTGCCC GCTGTGAGGT AAATGTGGAT GACTGCCTGA TGCGGCCTTG TGCTAACGGT V G A R C E V N V D D C L M R P C A N G
25	541	GCCACCTGCC TTGACGGCAT AAACCGCTTC TCCTGCCTCT GTCCTGAGGG CTTTGCTGGA A T C L D G I N R F S C L C P E G F A G
35	601	CGCTTCTGCA CCATCAACCT GGATGACTGT GCCAGCCGCC CATGCCAGAG AGGGGCCCGC R F C T I N L D D C A S R P C Q R G A R
40	661	TGTCGGGACC GTGTCCATGA CTTCGACTGC CTCTGCCCCA GTGGCTATGG TGGCAAGACT C R D R V H D F D C L C P S G Y G G K T
	721	TGTGAGCTTG TCTTACCTGT CCCAGACCCC CCAACCACAG TGGACACCCC TCTAGGGCCC C E L V L $\stackrel{\circ}{P}$ V P D P P T T V D T P L G P
45	781	ACCTCAGCTG TAGTGGTACC TGCCAC GGGG CCAGCCCCCC ACAGCGCAGG GGCTGGTCTG T S A V V V P A T G P A P H S A G A G L
50	841	CTGCGGATCT CAGTGAAGGA GGTGGTGCGG AGGCAAGAGG CTGGGCTAGG TGAGCCTAGC L R I S V K E V V R R Q E A G L G E P S
50	901	TTGGTGGCCC TGGTGGTGTT TGGGGCCCTC ACTGCTGCCC TGGTTCTGGC TACTGTGTTG L V A L V V F G A L T A A L V L A T V L
55	961	CTGACCCTGA GGGCCTGGCG CCGGGGTGTC TGCCCCCCTG GACCCTGTTG CTACCCTGCC L T L R A W R R G V C P P G P C C Y P A
	1021	CCACACTATG CTCCAGCGTG CCAGGACCAG GAGTGTCAGG TTAGCATGCT GCCAGCAGGG PHYAPACQDQ ECQVSMLPAG
60	1081	. CTCCCCCTGC CACGTGACTT GCCCCCTGAG CCTGGAAAGA CCACAGCACT G L P L P R D L P P E P G K T T A L

- 7/36 -

Figure 6:
Alignment of predicted amino acid sequence of SCS0009 with SCS0009-SV3

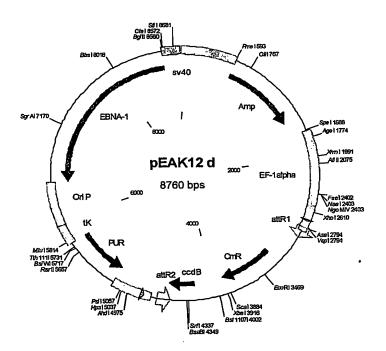
5	SCS0009	MPSGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC
	scs0009sv3	MPSGCRCLHLVC LLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC
10	scs0009 scs0009sv3	VRMPGCQHGTCHQPWQCICHSGWAGKFCDKGFHGR VRMPGCQHGTCHQPWQCICHSGWADEHICTTQSPCQ NGGQCMYDGGGEYHCVCLPGFHGR
15	scs0009 scs0009sv3	DCERKAGPCEQAGSPCRNGGQCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANG DCERKAGPCEQAGSPCRNGGQCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANG
	scs0009 scs0009sv3	ATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKT ATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKT
20	scs0009 scs0009sv3	CELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEAGLGEPS CELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEAGLGEPS ************************************
25	scs0009 scs0009sv3	LVALVVFGALTAALVLATVLLTLRAWRRGVCPPGPCCYPAPHYAPACQDQECQVSMLPAG LVALVVFGALTAALVLATVLLTLRAWRRGVCPPGPCCYPAPHYAPACQDQECQVSMLPAG
30	scs0009 scs0009sv3	LPLPRDLPPEPGKTTAL ***********************************

- 8/36 -

Figure 7:

Map of expression vector pEAK12d pEAK12 d, 8760 bps DNA Circular Molecule: pEAK12DEST.cm5 File Name: Mammalian cell expression vector (plasmid ID 11345) 5 Description: Molecule Features: Description Туре Start End Name pmb -ori REGION 595 GENE 596 1519 Amp 1690 2795 EF -lalpha REGION REGION 2703 2722 2845 2796 REGION 2855 attR1 MARKER 3915 3256 CmR GENE

10 position of pEAK12F primer MCS 15 4562 ccdB GENE 4257 C attR2 MARKER 4603 MCS REGION 4733 4733 poly A/splice 4734 5162 REGION position of pEAK12R primer REGION 4819 4848 C 20 5781 5163 C PUR PUROMYCIN GENE 5782 C tK tK promoter REGION 6005 6006 C Ori P 6500 REGION 6500 C EBNA -1 8552 GENE sv40 REGION 8553 8752

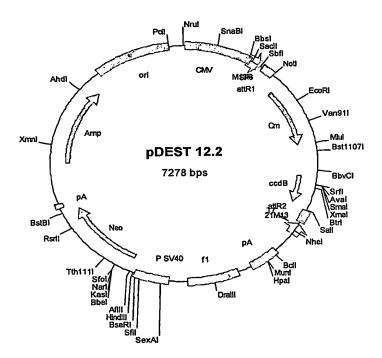


- 9/36 -

Figure 8:

Map of Expression vector pDEST12.2

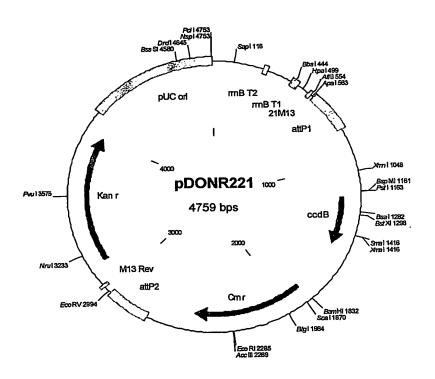
	Molecule	:	pDEST 12	.2, 7278	bps	DNA Circular	
	File Nam	e:	pDEST12 -	-2.cm5			
5	Descript	ion:	Euk aryor	ic expres	sion		
	Type	Start	End	Name		Description	
	REGION	15	608	CMV		CMV promoter	
	MARKER	648		M13R		M13R primer	
	REGION	687	706	SP6		SP6 promoter	
10	REGION	730	854	at tR1			
	GENE	963	1622	Cm			
	GENE	1964	2269	ccdB			
	REGION	2310	2434	attR2			
	GENE	2484	2464 C	T7		T7 promoter	
15	MARKER	2512	C	21M13		21M13 primer	
	REGION	2784	3050	рA		SV40 polyadenylation signal	
	REGION	3176	3631	f1		fl intergenic region	
	REGION	3791	4099	P SV40		SV40 ori & early promoter	
	GENE	4158	4952	Neo			_
20	REGION .	5016	5064	pΑ		synthetic poly adenylation sign	al
	GENE	5475	6335	Amp			
	REGION	6480	7153	ori		pUC ori	



- 10/36 -

Figure 9
Map of pDONR 221

	Molecule	:		DNA Circular					
	File Nam	ne:	pDONR221.cm5, dated 03 Jun 2003						
5	Descript	ion:							
	Type	Start	End Name	Description					
	REGION	295	268 C rrnB T2	transcription termination sequence					
	REGION	470	427 C rrnB Tl	transcription termination sequence					
	REGION	536	553 21M13	M13 Forward primer					
10	REGION	570	801 attPl						
	GENE	1197	1502 ccdB						
	GENE	1844	2503 Cm r	Chloramphenicol resistance gene					
	REGION	2751	2982 attP2	-					
	REGION	3040	3023 C M13 Rev	M13 Reverse primer					
15	GENE	3153	3962 Kan r						
	REGION	4083	4756 pUC ori						

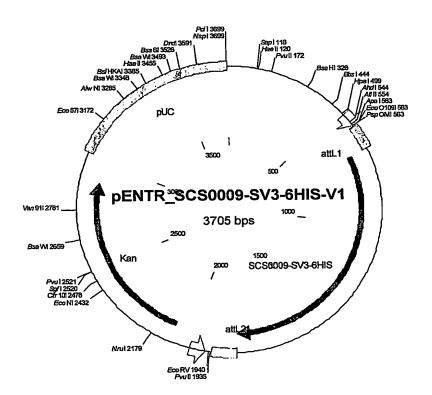


- 11/36 -

Figure 10

Map of pENTR-SCS0009SV3-6HIS

5	Molecule: File Name: Description:		pENTR_SCS0009 -SV3-6HIS-V1, 3705 bps DNA Circula 14879[1].cm5 Ligation of SCS0009 -SV3-6HIS into pdonr221					
•	•	Start	End	Name	Descri			
	туре		Bild	Monic				
	MARKER	536			21M13	Forward p	rimer	
	REGION	568	670	attLl				
	GENE	677	1825	SCS0009	9 -SV3-6HIS			
10	REGION	1829	1930	attL2				
	MARKER	1986	C	;		everse pr		
	GENE	2099	2908	Kan		cin resis	tance	gene
	REGION	3029	3702	pUC	pUC or	igin		

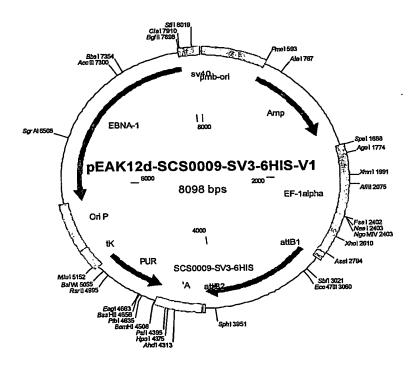


- 12/36 -

Figure 11

Map of pEAK12d-SCS0009SV3-6HIS

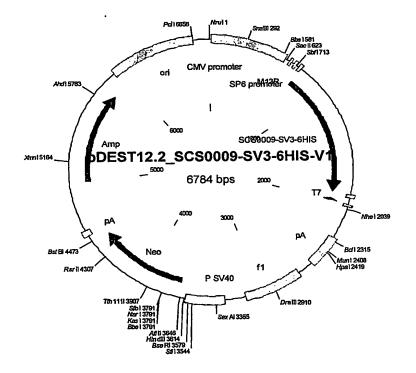
	Molecule	:	pEAK12d	-scs000	9-SV3-6	HIS-V1,	809	8 bps	DNA Ci	rcul	ar		
5	File Name: Description:		14885[1].cm5 pEAK12 DES with two		two re	combinat	ion	sites	attR1	and	attR2	between	n
	which the	e cDNA											
	Type	Start	End	Name		Descript	ton						
	REGION	2	595	pmb -o	ri								
10	GENE	596	1519	Amp									
	REGION	1690	2795	EF -la	lpha								
	REGION	2796	2845			MCS''							
	REGION	2855	2874	attB1									
	GENE	2888	4039	SCS000)9 -SV3-	·6HIS							
	REGION	4044	4065	attB2									
15	REGION	4071	4071			'MCS							
	REGION	4072	4500	'A		poly A/s	splic	ce					
	GENE	5119	4501	C PUR		PUROMYCI	IN						
	REGION	5343	5120	C tK		tK promo	oter						
	REGION	5838	5344	C Ori P									
20	GENE	7890	5838	C EBNA -	1								
	REGION	7891	8090	sv 40									



- 13/36 -

Figure 12

	Map of p	DEST12.	2 -SCS0009	SV3-6HIS	
	Molecule	:	pDEST12.	2_SCS0009 -SV3	8-6HIS-V1, 6784 bps DNA Circular
	File Nam	ie:	14889[1]	.cm5	
5	Descript	ion:	Ligation		SV3-6HIS-V1 into pDEST 12.2
	Туре	Start	End	Name	Description
	REGION	15	608	CMV promoter	
	REGION	648	665	M13R	Forward primer
	REGION	687	706	SP6 promoter	
10	REGION	730	756	attB1	
	GENE	763	1911	scs0009 -sv3-	-6HIS
	REGION	1940	1915 C	at tB2	
	GENE	1990	1970 C	T 7	T7 promoter
	REGION	2018	2001 C		21M13 reverse primer
15	REGION	2290			SV40 polyadenylation signal
	REGION	2682			fl intergenic region
	REGION	3297	3605	P SV40	SV40 ori & early promoter
	GENE	3664	4458	Neo	
	REGION	4522	4570	pΆ	synthetic poly adenylation signal
20	GENE	4981	5841	Amp	
	REGION	5986	6659	ori	pUC ori



PCT/EP2003/051092

- 14/36 -

Figure 13

the second section of the second second

Nucleotide sequence of SCS0009 prediction with translation

5	1 61 · 121	AGACGGCAAC GTGGACAGGA AGAAGCGGAG GGCGAGGAGG AGCAGAGGAG CACACAGATG AAGCAGGTGT CCACGGGTCC GGCCGTCCAT CCGTCCGTCC CTCCTGGGGC CGGCGCTGAC CATGCCCAGC GGCTGCCGCT GCCTGCATCT CGTGTGCCTT TTGTGCATTC TGGGGGCTCC M P S G C R C L H L V C L L C I L G A
10	181	CGGTCAGCCT GTCCGAGCCG ATGACTGCAG CTCCCACTGT GACCTGGCCC ACGGCTGCTG P G Q P V R A D D C S S H C D L A H G C
	241	TGCACCTGAC GGCTCCTGCA GGTGTGACCC GGGCTGGAG GGGCTGCACT GTGAGCGCTG C A P D G S C R C D P G W E G L H C E R
15	301	TGTGAGGATG CCTGGCTGCC AGCACGGTAC CTGCCACCAG CCATGGCAGT GCATCTGCCAC C V R M P G C Q H G T C H Q P W Q C I C
20	361	CAGTGGCTGG GCAGGCAAGT TCTGTGACAA AGGCTTCCAT GGGCGTGACT GCGAGCGCAA H S G W A G K F C D K G F H G R D C E R
	421	GGCTGGACCC TGTGAACAGG CAGGCTCCCC ATGCCGCAAT GGCGGGCAGT GCCAGGACGA K A G P C E Q A G S P C R N G G Q C Q D
25	481	CCAGGGCTTT GCTCTCAACT TCACGTGCCG CTGCTTGGTG GGCTTTGTGG GTGCCCGCTG D Q G F A L N F T C R C L V G F V G A R
	541	TGAGGTAAAT GTGGATGACT GCCTGATGCG GCCTTGTGC T AACGGTGCCA CCTGCCTTGAC E V N V D D C L M R P C A N G A T C L
30	601	CGGCATAAAC CGCTTCTCCT GCCTCTGTCC TGAGGGCTTT GCTGGACGCT TCTGCACCAT D G I N R F S C L C P E G F A G R F C T
35	661	CAACCTGG AT GACTGTGCCA GCCGCCCATG CCAGAGAGGG GCCCGCTGTC GGGACCGTGT I N L D D C A S R P C Q R G A R C R D R
	721	CCACGACTTC GACTGCCTCT GCCCCAGTGG CTATGGTGGC AAGACCTGTG AGCTTGTCTT V H D F D C L C P S G Y G G K T C E L V
40	781	ACCTGTCCCA GACCCCCCAA CCACAGTGGA CACCCCTCTA GGGCCCACCT CAGCTGTAGT L P V P D P P T T V D T P L G P T S A V
	841	GGTACCTGCC ACGGGGCCAG CCCCCACAG CGCAGGGGCT GGTCTGCTGC GGATCTCAGT V V P A T G P A P H S A G A G L L R I S
45	901	GAAGGAGGTG GTGCGGAGGC AAGAGGCTGG GCTAGGTGAG CCTAGCTTGG TGGCCCTGGT V K E V V R R Q E A G L G E P S L V A L
50	961	GGTGTTTGGG GCCCTCACTG CTGCCCTGGT TCTGGCTACT GTGTTGC TGA CCCTGAGGGC V V F G A L T A A L V L A T V L L T L R
	1021	CTGGCGCCGG GGTGTCTGCC CCCCTGGACC CTGTTGCTAC CCTGCCCCAC ACTATGCTCC A W R R G V C P P G P C C Y P A P H Y A
55	1081	AGCGTGCCAG GACCAG GAGT GTCAGGTTAG CATGCTGCCA GCAGGGCTCC CCCTGCCACG P A C Q D Q E C Q V S M L P A G L P L P
60	1141	TGACTTGCCC CCTGAGCCTG GAAAGACCAC AGCACTGTGA TGGAGGTGGG GGCTTTCTGG R D L P P E P G K T T A L
60	1201 1261	TO THE RESIDENCE OF THE PROPERTY OF THE PROPER

THE MAN TO SERVICE STATE OF THE SERVICE STATE OF TH

PCT/EP2003/051092

- 15/36 -

	1321	ACAGAATGTA	AGATGGAATT	TTATCAAATA	AAACTATGAA	AATGCAAGTG	GGCTCCTATG
	1381	CCAGAAAAAC	CCACCTGGCG	TTCCAGATGC	AAGAGGGCCA	GAGCAGAGGC	CTGGTTCTGG
	1441	GGAAGCCTCA	GGATGCTGCC	CACCAAGGAG	TGATTTCCAA	AGAGTAATCC	AGGGTGCCCT
	1501	TTTCCCTTCT	GGGGAAGTGT	GGAGAGGTAG	AGCCCCAGAG	GAGAATGTAA	ACAAGCAGCC
5	1561	AGCACCTCTG	TATAGGCCCG	GCCTGGATCA	GAGAGAGGGG	AGAACTCTGC	AGGGTGTGGG
	1621	ATTGGGC TCA	GGGACCTCCG	AGTGAGGCAG	GGACTCCCTG	CTG	

- 16/36 -

Figure 14

Nucleotide sequence with translation of cDNA insert in image clone 3349698 (SCS0009 -SV4)

5	1	ATGC	CCA	GCG	GCT	GCC	GCTG	CC	rgc.	ATC'	TC	GT(GTG	CC.	rgr	TGT	CA'	PTCT	GGG	افافاد	JICC	·C
•		M	P	s	G	С	R	С	L	H	1	•	V	С	L	L	С	I	L	G	A	P
	61	GGTC	AGC	CTG	TCC	GAG	CCGA	TG.	ACT	GCA	GC	TC	CCF	CTC	STG	ACC!	rgge	CCCA	CG	CT	GCTG	T
10		G	Q	P	V	R	A	D	D	С	S		S	Н	С	D	L	A	H	G	С	Ç
10	121	GCAC	CTG	ACG	GCT	CCT	GCAG	GT	GTG	ACC	CG	GG	CTO	GG:	AGG	GGC'	rgc.	ACTG	TG	AGC	GCT	T
		A	P	D	G	S	С	R	С	D	P		G	W	E	G	L	н	С	E	R	С
	181	GTGA	GGA	TGC	CTG	GCT	GCCA	GC	ACG	GTA	cc	TG	CCZ	ACC.	AGC	CAT	GGC	agtg	CA	TCT	GCC	4C
15		V	R	M	P	G	С	Q	H	G	T		С	H	Q	P	W	Q	С	I	С	Н
	241	AGTG	GCT	GGG													TGT.					
		s	G	M	A	G	K	F	С	D	K		D	E	H	I	С	T	T	Q	S	P
20	301	TGCC	AGA	ATG	GAG	GCC	AGTG	CA	TGI	'ATG	AC								TG	TGT	GCT'	ΓA
		С	Q	N	G	G	Q	С	M	Y	D	•	G	G	G	E	Y	Н	С	V	С	L
	361	CCAG	GC?	TCC	: AT	GGG	CGTGF	C	rgco	SAG	CGC	: A7	AGG	CTG	GAC							
25		P	G	F	H	G	R	D	С	Ē	P	t	K	A	G	P						

5

PCT/EP2003/051092

- 17/36 -

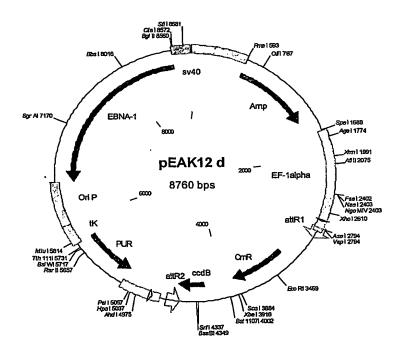
Figure 15

Alignment of predicted amino acid sequence of SCS0009 with SCS0009-SV4

	SCS0009 SCS0009SV4	MPSGCRCLHLVCILCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDP MPSGCRCLHLVCILCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDP
10	SCS0009 SCS0009SV4	GWEGLHCERCVRMPGCQHGTCHQPWQCICHSGWAGKFCDKGWEGLHCERCVRMPGCQHGTCHQPWQCICHSGWAGKFCDKDEHICTTQSP
15	SCS0009 SCS0009SV4	CQNGGQCMYDGGGEYHCVCLPGFHGRDCERKAGPCEQAGSPCRNGGQCQD
	scs0009 scs0009sv4	DQGFALNFTCRCLVGFVGARCEVNVDDCLMRPCANGATCLDGINRFSCLC
20	scs0009 scs0009sv4	PEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPSGYGGKTCELV
	SCS0009 SCS0009SV4	LPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEA
25	scs0009 scs0009sv4	GLGEPSLVALVVFGALTAALVLATVLLTLRAWRRGVCPPGPCCYPAPHYA
30	SCS0009 SCS0009SV4	PACQDQECQVSMLPAGLPLPRDLPPEPGKTTAL

- 18/36 -

	Figure 1	6									
	Map of e	xpressi	on vecto	r pEAK12	d						
	Molecule	:	pEAK12	pEAK12 d, 8760 bps DNA Circular							
	File Nam	e:		pEAK12DEST.cm5							
5	Descript	ion:	Mammali	an cell	expression vector (plasmid ID 11345)						
	Molecule	Featur	es:								
	Type	Start	End	Name	Description						
	REGION	2	595		pmb -ori						
	GENE	596	1519	Amp							
10	REGION	16 90	2795	EF-1a:							
	REGION	2703	2722		position of pEAK12F primer						
	REGION .	2796	2845		MCS						
	MARKER	2855		attR1							
	GENE	3256	3915	CmR							
15	GENE	4257	4562	ccdB							
	MARKER	4603		C attR2							
	REGION	4733			MCS						
	REGION		5162		poly A/splice						
	REGION	4819	4848	С	position of pEAK12R primer						
20	GENE	5781	5163		PUROMYCIN						
	REGION	6005	5782	C tK	tK promoter						
	REGION	6500		C Ori P							
-	GENE	8552		C EBNA -	1						
	REGION	8553	8752	sv40							

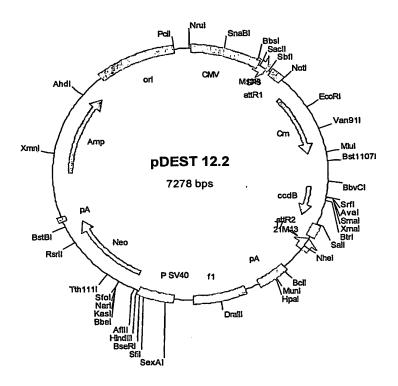


- 19/36 -

Figure 17

Map of Expression vector pDEST12.2

	-	-						
	Molecule	:			bps	DNA Circular		
	File Name	e:	pDEST12 -2.cm5					
5	Descript:	ion:	Eukaryoric expression			vector		
	Type	Start	End	Name		Description		
	REGION	15	608	CMV		CMV promoter		
	MARKER	648		M13R		M13R primer		
	REGION	687	706	SP6		SP6 promoter		
10	REGION	730	854			•		
10	GENE	963						
	GENE	1964						
		2310	2434					
	REGION		_			T7 promoter		
1.5	GENE	2484				21M13 primer		
15	MARKER	2512		C 21M13				
	REGION	2784		pΑ		SV40 polyadenylation signal		
	REGION	3176	3631			fl intergenic region		
	REGION	3791	4099	P SV40		SV40 ori & early promoter		
	GENE	4158	4952	Neo				
20	REGION	5016	5064	pΆ		synthetic poly adenylation signal		
	GENE	5475	6335	Amp				
	REGION	6480	7153	ori		pUC ori		

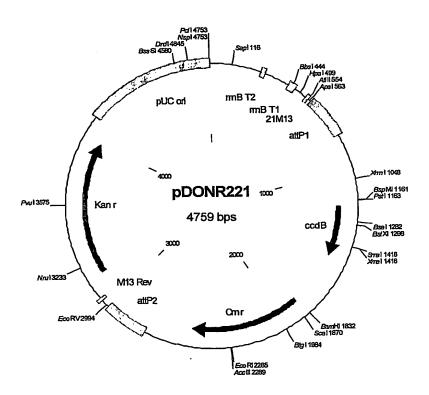


- 20/36 -

Figure 18

Map of pDONR 221

5	Molecule: File Name: Description:		pDONR221, 4759 bps DNA Circular pDONR221.cm5, dated 03 Jun 2003					
_	Type	Start	End Name	Description				
	REGION	295	268 C rrnB T2	transcription termination sequence				
	REGION	470	427 C rrnB T1	transcription termination sequence				
10	REGION	536	553 21M13	M13 Forward primer				
	REGION	570	801 attP1					
	GENE	1197	1502 ccdB					
	GENE	1844	2503 Cm r	Chloramphenicol resistance gene				
	REGION	2751	2982 attP2					
	REGION	3040	3023 C M13 Rev	M13 Reverse primer				
15	GENE	3153	3962 Kan r					
	REGION	4083	4756 pUC ori					

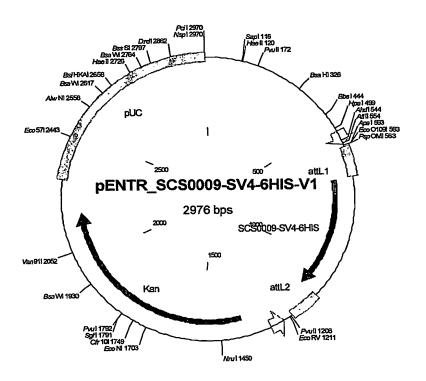


- 21/36 -

Figure 19

Map of pENTR-SCS0009SV4-6HIS

5	Molecule: File Name: Description:		pENTR_SCS0009-SV4-6HIS-V1, 2976 bps DNA Circula 15055[1].cm5 Ligation of SCS0009-SV4-6HIS into pdonr221					
	Type	Start	End	Name	Description `			
	MARKER	536			21M13 Forward primer			
	REGION	568	670	attLl				
	GENE	677	1096	SCS0009 -	SV4-6HIS			
10	REGION	1100	1201	attL2				
	MARKER	1257	С		M13 Reverse primer			
	GENE	1370	2179	Kan	Kanamycin resistance gene			
	REGION	2300	2973	pUC	pUC origin			

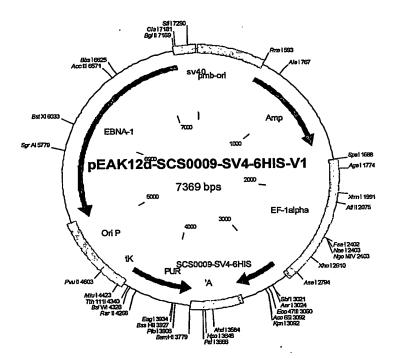


- 22/36 -

Figure 20

Map of pEAK12d-SCS0009SV4-6HIS

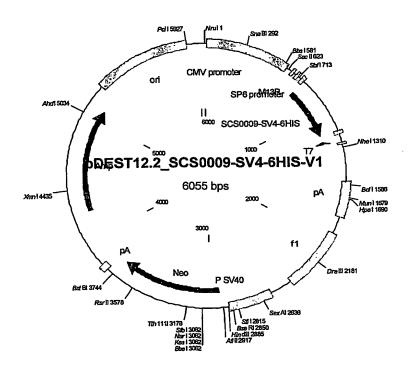
	Molecule	:	pEAK12d	-scs0009-sv	4-6HIS-V1, 7369 bps DNA Circular					
		File Name:		15061[1].cm5						
5	Descript		pEAK12	ES with two	recombination sites attR1 and attR2 between					
	which the cDNA		is inserted							
	Type	Start	End	Name	Description					
	REGION	2	595	pmb -ori						
	GENE	596	1519	Amp						
10	REGION	1690	2795	EF -lalpha						
	REGION	2796	2845		MCS''					
	REGION	2855	2874		attB1					
	GENE	2888	3310	scs0009 -						
	REGION	3315	3336		attB2					
15	REGION	3342	3342		'MCS					
	REGION	3343	3771	'A	poly A/splice					
	GENE	4390	3772	C PUR	PUROMYCIN					
	REGION	4614	4391	C tK	tK promoter					
	REGION	5109		C Ori P						
20	GENE	7161		C EBNA-1						
	REGION	7162	7361	sv40						



- 23/36 -

Figure 21

	i iguio z i									
	Map of p	DEST12	2.2-SCS00	009SV4-6HIS						
	Molecule	:	pDEST12.	pDEST12.2_SCS0009 -SV4-6HIS-V1, 6055 bps DN						
	File Nam	e:		15063[1].cm5						
5	Descript	ion:	Ligation	Ligation of SCS0009 -SV4-6HIS-V1 into pDEST 12						
	Type	Start	End	Name	Description					
	REGION	15	608	CMV promoter						
	REGION	648	665	M13R	Forward primer					
	REGION	687	706	SP6 promoter						
10	REGION	730	756		attB1					
	GENE	763	1182	SCS0009 -SV4-	-6HIS					
	REGION	1211	1186 C		attB2					
	GENE	1261	1241 C	T 7	T7 promoter					
	REGION	1289	1272 C		21M13 reverse primer					
15	REGION	1561	1827	pA	SV40 polyadenylation signal					
	REGION	1953	2408	f1	fl intergenic region					
	REGION	2568	2876	P SV40	SV40 ori & early promoter					
	GENE	2935	3729	Neo						
	REGION	3793	3841	pΑ	synthetic poly adenylation signal					
20	GENE	4252	5112	Amp						
	REGION	5257	5930	ori	pUC ori					



PCT/EP2003/051092

- 24/36 -

Figure 22
Nucleotide sequence of SCS0009 prediction with translation

5	1 61 121	agacggcaac gtggacagga agaagcggag ggcgaggagg agcagaggag cacacagatg aagcaggtgt ccacgcgtcc ggccgtccat ccgtccgtcc ct cctggggc cggcgctgac catgcccagc ggctgccgct gcctgcatct cgtgtgcctg ttgtgcattc tgggggctcc m p s g c r c l h l v c l l c i l g a
10	181	cggtcagcct gtccgagccg atgactgcag ctcccactgt gacctggccc acggctgctg p g q p v r a d d c s s h c d l a h g c
	241	tgcacctgac ggctcctgca ggtgtgaccc gggctggag gggctgcact gtgagcgctg c a p d g s c r c d p g w e g l h c e r
15	301	tgtgaggatg cctggctgcc agcacggtac ctgccaccag ccatgg cagt gcatctgcca c v r m p g c q h g t c h q p w q c i c
20	361	cagtggctgg gcaggcaagt tctgtgacaa aggcttccat gggcgtgact gcgagcgcaa h s g w a g k f c d k g f h g r d c e r
20	421	ggctggaccc tgtgaacagg caggctcccc atgccgcaat ggcgggcagt gccaggacga ${f k}$ a ${f g}$ ${f p}$ c ${f q}$ a ${f g}$ ${f s}$ ${f p}$ c ${f r}$ ${f n}$ ${f g}$ ${f q}$ c ${f q}$ d
25	481	ccagggettt geteteaact teaegtgeeg etgettggtg ggetttgtgg gtgeeegetg d q g f a l n f t c r c l v g f v g a r
	541	tgaggtaaat gtggatgact gcctgatgcg gccttgtgct aacggtgcca cctgccttga c e v n v d d c l m r p c a n g a t c l
30	601	cggcataaac cgcttctcct gcctctgtcc tgagggcttt gctggacgct tctgcaccat d g i n r f s c l c p e g f a g r f c t
25	661	caacctggat gactgtgcca gccgcccatg ccagagaggg gcccgctgtc gggaccgtgt i n l d d c a s r p c q r g a r c r d r
35	721	ccacgacttc gactgcctct gccccagtgg ctatggtggc aagacctgtg agct tgtctt v h d f d c l c p s g y g g k t c e l v
40	781	acctgtccca gaccccccaa ccacagtgga cacccctcta gggcccacct cagctgtagt l p v p d p p t t v d t p l g p t s a v
	841	ggtacetgce aeggggeeag eec eecacag egcagggget ggtetgetge ggateteagt $v \ v \ p \ a \ t \ g \ p \ a \ p \ h \ s \ a \ g \ a \ g \ l \ l \ r \ .i \ s$
45	901	gaaggaggtg gtgcggaggc aagaggctgg gctaggtgag cctagcttgg tggccctggt v k e v v r r q e a g l g e p s l v a l
	961	ggtgtttggg gccctcactg ctgccctggt tctggctact gtgttgctga ccctgagggc v v f g a l t a a l v l a t v l l t l r
50	1021	ctggcgccgg ggtgtctgcc cccctggacc ctgttgctac cctgccccac actatgctcc a w r r g v c p p g p c c y p a p h y a
55	1081	agegtgeeag gaccaggagt gteaggttag catgetgeea geagggetee ecetgeeacg p a c q d q e c q v s m l p a g l p l p

PCT/EP2003/051092

- 25/36 -

	1141	tgacttgccc r d l p	cctgagcctg p e p	gaaagaccac g k t	agcactgtga t a l	tggaggtggg	ggctttctgg
	1201	coccttcct	cacctettee	acceteaga	ctggagtggt	ccatteteae	caccetteag
_			Caccecce	accececage	ccaacacaac		
5	1261	cttgggtaca	cacacagagg	agacctcagc	ctcacaccag	aaatattatt	tttttaatac
	1321	acagaatgta	agatggaatt	ttatcaaata	aaactatgaa	aatgcaagtg	g gctcctatg
	1381	ccagaaaaac	ccacctggcg	ttccagatgc	aagagggcca	gagcagaggc	ctggttctgg
	1441	ggaagcctca	ggatgctgcc	caccaaggag	tgatttccaa	agagtaatcc	agggtgccct
	1501	tttcccttct	ggggaagtgt	ggagaggtag	agccccagag	gagaatgtaa	acaagcagcc
10	1561	agcacctctg	tataggcccg	g gcctggatca	gagagagggg	agaactctgc	agggtgtggg
	1621	attoggetea	gggacctcco	agtgaggcag	ggactccctg	cta	

- 26/36 -

Figure 23

5

Nucleotide sequence with translation of SCS0009-SV5 PCR product indicating the positions of the SCS0009-AP1, -AP2, -AP3 and -AP4 primers used to generate the SCS0009 sequence.

		SCS0009-AP1
10	1	tccatccgtc cgtccctcct ggggccggcg ctgaccatgc ccagcggctg ccgctgcctg $$\tt m$$ p s g c r c l
15	61	catchegtgt gootgttgtg cattctgggg gotcoeggte agcotgteeg agc cgatgac h l v c l l c i l g a p g q p v r a d d
	121	tgcagctccc actgtgacct ggcccacggc tgctgtgcac ctgacggctc ctgcaggtgt c s s h c d l a h g c c a p d g s c r c
20	181	gacccgggct gggaggggct gcactgtgag cgctgtgtga ggatgcctgg ctgccagcac d p g w e g l h c e r c v r m p g c q h
25	241	ggtacctgcc accagccatg gcagtgcatc tgccacagtg gctgggcagg caagttctgt g t c h q p w q c i c h s g w a g k f c
30	301	gacaaagatg aacatatetg taccacgeag tececetgee agaatggagg eeagtgeatg $\begin{array}{cccccccccccccccccccccccccccccccccccc$
	361	tatgacgggg gcggtgagta ccattgtgtg tgcttaccag gcttccatgg gcgtgactgc y d g g g e y h c v c l p g f h g r d c
35	421	gagcgcaagg ctggaccctg tgaacaggca ggctccccat gccgcaatgg cgggcagtgc e r k a g p c e q a g s p c r n g g q c
40	481	caggacgacc agggetttge teteaactte acgtgeege t gettggtggg etttgtgggt q d d q g f a l n f t c r c l v g f v g
	541	gcccgctgtg aggtaaatgt ggatgactgc ctgatgcggc cttgtgctaa cggtgccacc a r c e v n v d d c $1\ m$ r p c a n g a t
45	601	tgccttgacg gcataaaccg cttctcctgc ctctgtcctg agggctttgc tggacgcttc c l d g i n r f s c l c p e g f a g r f
	661	tgcaccatca acctggatga ctgtgccagc cgcccatgcc agagaggggc ccgctgtcgg c t i n l d d c a s r p c q r g a r c r
50	721	gaccgtgtcc acgacttcga ctgcctctgc cccagtggct atggtggcaa gacctgtgag drvhdf dclcpsgyggktce
55	781	cttgtcttac ctgtcccaga ccccccaacc acagtggaca cccctctagg gcccacctca l v l p v p d p p t t v d t p l g p t s

- 27/36 -

	841	gctgtagtgg	tacctgccac	ggggccagcc	ccccacagcg	caggggctgg	tctgctgcgg
		a v v	v p a	t g p a	p h s	a g a	gllr
5	901	atctcagtga i s v	aggaggtggt k e v		gagg ctgggd e a g		
	961	gccctggtgg . a l v	tgtttggggc v f g	cctcactgct a l t a	gccctggttc a l v	tggctactgt l a t	gttgctgacc v l l t
10	1021	ctgagggcct l r a	ggcgccgggg wrr			gttgctaccc c c y	
15	1081	tatgctccag y a p	g cgtgccagga a c q	ccaggagtgt d q e c	caggttagca q v s	tgctgccagc m l p	agggctcccc a g l p
	1141	ctgccacgto l p r	d l p	реро	aagaccacag k t t	cactgtgatg a l	gaggtgggg
20							

Sequence in grey = bases not present in SCS0009 prediction

- 28/36 -

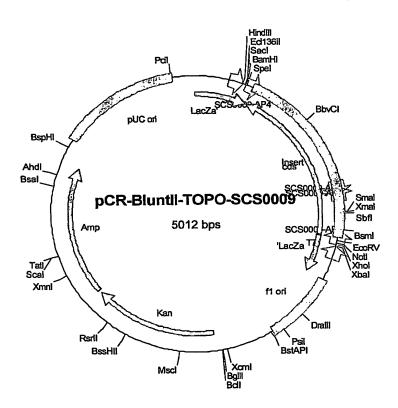
Figure 24

	Nucleoti 1	de sequence accatgece m p	a gcgg	ctgccg	n of clo ctgcct r c	gcat	CS0009 OR ctcgtgtgc 1 v c	c tgttgtgcat	tctgggggct i l g a
5	61	p g c				ctgc d c	agctcccac s s h	t gtgacctggc c d l	ccacggct gc a h g c
10	121	tgtgcacct c a p			caggtg c r		p g w	g aggggctgca e g l	ctgtgagcgc h c e r
	181					acggt h g	acctgccad t c h	c agccatggca q p w	gtgcatctgc q c i c
15	241	cacagtgge h s				gtgac c d	aaaggctto k g f	c atgggcgtga h g r	ctgcgagcgc d c e r
20	301	aaggctgg k a			ggcago q a		ccatgccgc p c r	a atggcgggca n g g	gtgccaggac q c q d
20	361	gaccaggg d q	_	tctcaa a l		egtgc t c		g tgggctttgt L v g f	gggtgcccgc v g a r
25	421			ggatga v d	ctgccf d c			g ctaacggtgo a n g	cacctgcctt a t c l
	481		aa acco	cttctc r f	ctgcc s c				ctt ctgcacc r f c t
30	541			ctgtgc d c	cagcc a s			ag gggcccgctg g a r	g tegggaeegt e r d r
35	601	gtccacga v h		actgcct d c	ctgcc l c			tg gcaagacct g g k t	g tgagcttgtc c e l v
33	661	ttacctgt l p		acccccc d p	aacca p t			tc tagggcccac p 1 g p	c ctcagctgta t s a v
40	7 <u>2</u> 1	gtggtacc v v		eggggcc t g	agccc p a			gg ctggtctgct g a g l	t gcggatctca l r i s
	781	gtgaagga v k		tgcggag v r		aggct e a		tg agcctagct g e p s	t ggtggccctg l v a l
45	841	gtggtgtt v v	_	-	tgctg t a	a 1	gttctggc v 1	ta ctgtgttgc a t v l	t gaccctgagg l t l r
50	901	gcctggcq a w		gtgtctg g v	c p	etgga p g	ccctgttg pc	ct accetgeee c y p a	c acactatgct p h y a
	961			accagga d q		aggtt q v		gc cagcagggc l p a g	t ccccctgcca l p l p
55	1021			ctgagc			c acagcact : t a	gt ga 1	

- 29/36 -

Figure 25
Map of pCR-BluntII-TOPO-SCS0009

	Molecule	:	pCR-Blu	ntII-TOPO-SCS	0009, 5012 bps DNA Circular
	Type	Start	End	Name	Description
5	GENE	1	336	LacZa'	LacZa gene
	MARKER	239		SP6	SP6 promoter
	MARKER	337		SCS0009 -AP4	
	MARKER	1107		SCS0009 -AP2	
	MARKER	1142	(C SCS0009 -AP3	SCS0009-AP3 primer site
10	GENE	1395	340 (C cds	SCS0009 cds
	REGION	1398	337 (C Insert	SCS0009 assembly PCR product
	MARKER	1398	(C SCS0009 -AP1	SCS0009-AP1 primer site
	GENE	1399	1650	'LacZa	LacZa gene
	MARKER	1487		С Т7	T7 promoter
15	REGION	1652	2066	fl ori	
	GENE	2400	3194	Kan	Kanamycin resistance ORF
	GENE	3212	4072	Amp	Ampicillin resistance ORF
	REGION	4217	4890	pUC ori	pUC origin

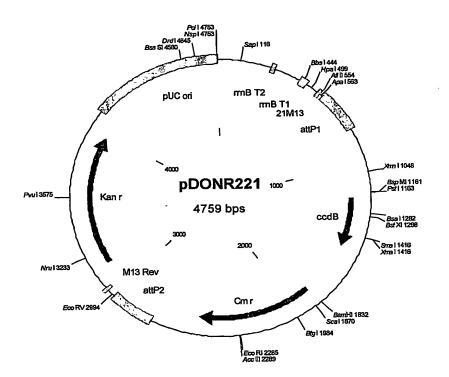


- 30/36 -

Figure 26

Map of pDONR 221

5	Molecule: File Name: Description:		pDONR221, 4759 bps pDONR221.cm5	3 DNA Circular		
•	Type	Start	End Name	Description		
	REGION	295	268 C rrnB T2	transcription termination sequence		
	REGION	470	427 C rrnB Tl	transcription termination sequence		
	REGION	536	553 21M13	M13 Forward primer		
10	REGION	570	801 attPl	•		
	GENE	1197	1502 ccdB			
	GENE	1844	2503 Cm r	Chloramphenicol resista nce gene		
	REGION	2751	2982 attP2			
	REGION	3040	3023 C M13 Rev	M13 Reverse primer		
15	GENE	3153	3962 Kan r			
	REGION	4083	4756 pUC ori			



- 31/36 -

Figure 27

Map of expression vector pEAK12d

Molecule: pEAK12 d, 8760 bps DNA Circular File Name: pEAK12DEST.cm5

5 Description: Mammalian cell expression vector (plasmid ID 11345)

Molecule Features: Description Start End Name Type REGION pmb -ori 595 596 15 19 GENE Amp EF -lalpha 10 2795 REGION 1690 position of pEAK12F primer REGION 2703 2722 REGION 2796 2845 MCS MARKER 2855 attR1 GENE 3256 3915 CmR 15 4562 ccdB 4257 GENE C attR2 MARKER 4603 4733 4733 REGION poly A/splice REGION 4734 5162 position of pEAK12R primer 4848 C REGION 4819 PUROMYCIN 20 GENE 5781 5163 C PUR REGION 6005 5782 C tK tK promoter 6500 6006 C Ori P REGION 8552 6500 C EBNA -1 GENE 8553 8752 sv40 REGION

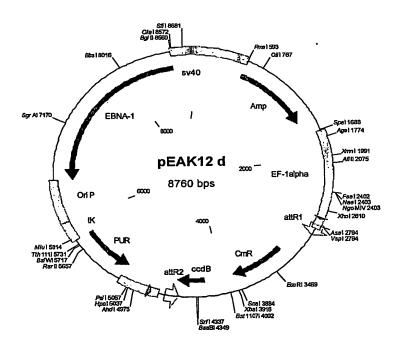
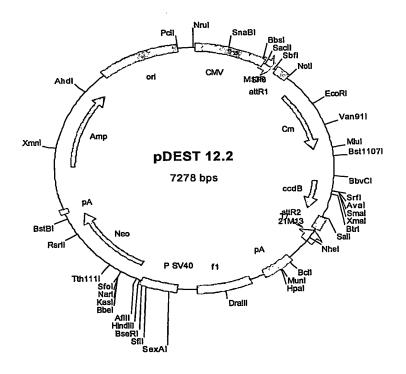


Figure 28

WO 2004/063222

	Molecule	:	pDEST 12	2.2, 7278	bps DNA Circular			
	File Nam	ie:	pDEST12 -2.cm5					
5	Descript	ion:	Eukaryor	cic express	ion vector			
	Type	Start	End	Name	Description			
	REGION	15	608	CMV	CMV promoter			
	MARKER	648		M13R	M13R primer			
	REGION	687	706	SP6	SP6 promoter			
10	REGION	730	854	attR1				
	GENE	963	1622	Cm				
	GENE	1964	2269	ccdB				
	REGION	2310	2434	attR2				
	GENE	2484	2464	C T 7	T7 promoter			
15	MARKER	2512	(C 21M13	21M13 primer			
	REGION	2784	3050	pΆ	SV40 polyadenylation signal			
	REGION	3176	3631	fl	fl intergenic region			
	REGION	3791	4099	P SV40	SV40 ori & early promoter			
	GENE	4158	4952	Neo				
20	REGION	5016	5064	pΑ	synthetic poly adenylation signal			
	GENE	5475	6335	Amp				
	REGION	6480	7153	ori	pUC ori			

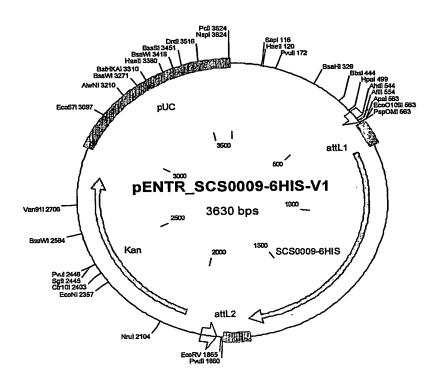


- 33/36 -

Figure 29

Map of pENTR-SCS0009-6HIS

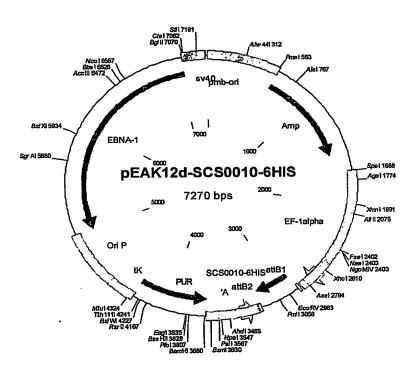
	Molecule: File Name: Description:		15057[1]	.cmS,	., 3630 bps DNA Circular
5			Ligation of SCS0009 -6HIS into pdonr221		
	Type	Start	End	Name	Description
	MARKER	536			21M13 Forward primer
	REGION	568	670	attL1	
	GENE	67 <i>1</i>	1750	SCS0009 -6HIS	5
10	REGION	1754	1855	attL2	
	MARKER	1911	С		M13 Reverse primer
	GENE	2024	2833	Kan	Kanamycin resistance gene
	REGION	2954	3627	pUC	pUC origin



- 34/36 -

Figure 30 Map of pEAK12d-SCS0009-6HIS

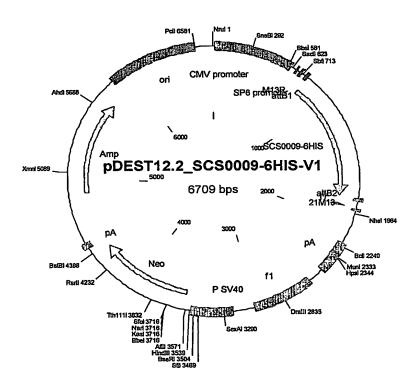
	Molecule	:	pEAK12d_	SCS0009 -6H	IS, 8023 bps DNA Circular
	File Nam	ne:	15062[1]		
5	Descript	ion:	pEAK12 D	ES with two	recombination sites attRl and attR2 between
	which th	e cDNA	is insert	ed	
	Туре	Start	End	Name	Description
	REGION	2	595	pmb -ori	
	GENE	596	1519	Amp	
10	REGION	1690	2795	EF -lalpha	
	REGION	2796	2845	MCS''	
	REGION	2855	2874	attB1	
	GENE	2888	3961	s cs0009-6	HIS
	REGION	3969	3990	attB2	
15	REGION	3996	3996	'MCS	
	REGION	3997		'A	poly A/splice
	GENE	5044			PUROMYCIN
	REGION	5268			tK promoter
	REGION	5763		C Ori P	
20	GENE	7815		EBNA -1	
	REGION	7816	8015	sv40	



- 35/36 -

Figure 31

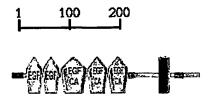
	Map of p	DEST1	2.2 - SCS00	09-6HIS	
	Molecule	:	pDEST12.2	2_SCS0009 - 6HI	(S-V1, 6709 bps DNA Circular
	File Nam		15064[1].		
5	Descript	ion:	Ligation	of SCS0009 -6	SHIS-V1 into pDEST 12.2
	Type	Start			Description
	REGION	15	608	CMV promoter	
	REGION	648	665	M13R	Forward primer
	REGION	687	706	SP6 promoter	
10	REGION	730	756	att B1	
	GENE	763	1836	SCS0009 -6HIS	5
	REGION	1865	1840 C	attB2	
	GENE	1915	1895 C	T 7	T7 promoter
	REGION	1943	1926 C	21M13	reverse primer
15	REGION	2215	2481	pA	SV40 polyadenylation signa 1
	REGION	2607	3062	f1	fl intergenic region
	REGION	3222	3530	P SV40	SV40 ori & early promoter
	GENE	3589	4383	Neo	
	REGION	4447	4495	pΑ	synthetic poly adenylation signal
20	GENE	4906	5766	Amp	
	REGION	5911	6584	ori	pUC ori



- 36/36 -

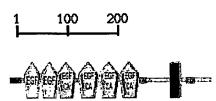
Figure 32

Domains within the query sequence SCS0009 of 352 residues



5

Domains within the query sequence SCS0009-SV3 of 377 residues



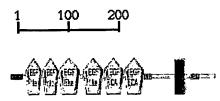
Domains within the query sequence SCS0009-SV4 of 134 residues 1 100 200



10



Domains within the query sequence SCS0009-SV5 of 383 residues is identical to sptremblnew|AAQ88493|AAQ88493



15

20

Transmembrane segments as pre dicted by the <u>TMHMM2</u> program (), coiled coil regions determined by the <u>Coils2</u> program () and Segments of low compositional compl exity, determined by the <u>SEG</u> program (), signal peptides determined by the <u>Sigcleave</u> program (), GPI anchors are indicated by (). Regions containing repeats detected by <u>Prospero</u>, but not covered by domains are indicated by ().

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

_	
☐ BLACK BORDERS	
\square image cut off at top, bottom or sides	
☐ FADED TEXT OR DRAWING	
BLURRED OR ILLEGIBLE TEXT OR DRAWING	
☐ SKEWED/SLANTED IMAGES	
☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS	
☐ GRAY SCALE DOCUMENTS	
☐ LINES OR MARKS ON ORIGINAL DOCUMENT	
☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY	

IMAGES ARE BEST AVAILABLE COPY.

☐ OTHER: __

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.